



PCT10

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,372

DATE: 11/06/2002 P.6
TIME: 15:30:16

Input Set : A:\65691270.app

Output Set: N:\CRF4\11062002\J049372.raw

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3 <110> APPLICANT: PITIOT, GILLES
4   LACAZETTE, ERIC
5   GACHON, FRANCOISE
7 <120> TITLE OF INVENTION: HUMAN ODORANT-BINDING PROTEINS WHICH BIND HYDROPHOBIC
8   LIGANDS: POLYPEPTIDES AND POLYNUCLEOTIDES ENCODING SAID
9   POLYPEPTIDES, AND USES THEREOF
11 <130> FILE REFERENCE: 065691/0270
13 <140> CURRENT APPLICATION NUMBER: 10/049,372
14 <141> CURRENT FILING DATE: 2002-02-12
16 <150> PRIOR APPLICATION NUMBER: PCT/FR00/02319
17 <151> PRIOR FILING DATE: 2000-08-11
19 <150> PRIOR APPLICATION NUMBER: FR 99 10439
20 <151> PRIOR FILING DATE: 1999-08-12
22 <160> NUMBER OF SEQ ID NOS: 53
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 676
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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33 <222> LOCATION: (43)..(552)
35 <220> FEATURE:
36 <223> OTHER INFORMATION: cDNA396 (676) /g1 (hOBPIIa-alpha)
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40                                     Met Lys Thr Leu
41                                     1
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44 Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Leu Ser Phe Thr Leu
45   5           10           15           20
47 gag gag gag gat atc aca ggg acc tgg tac gtg aag gcc atg gtg gtc      150
48 Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys Ala Met Val Val
49           25           30           35
51 gat aag gac ttt ccg gag gac agg agg ccc agg aag gtg tcc cca gtg      198
52 Asp Lys Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys Val Ser Pro Val
53           40           45           50
55 aag gtg aca gcc ctg ggc ggt ggg aac ttg gaa gcc acg ttc acc ttc      246
56 Lys Val Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala Thr Phe Thr Phe
57           55           60           65
59 atg agg gag gat cgg tgc atc cag aag aaa atc ctg atg cgg aag acg      294
60 Met Arg Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu Met Arg Lys Thr
61           70           75           80

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63 gag gag cct ggc aaa ttc agc gcc tat ggg ggc agg aag ctc ata tac 342
64 Glu Glu Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg Lys Leu Ile Tyr
65 85 90 95 100
67 ctg cag gag ctg ccc ggg acg gac gac tac gtc ttt tac tgc aaa gac 390
68 Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe Tyr Cys Lys Asp
69 105 110 115
71 cag cgc cgt ggg ggc ctg cgc tac atg gga aag ctt gtg ggt agg aat 438
72 Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu Val Gly Arg Asn
73 120 125 130
75 cct aat acc aac ctg gag gcc ctg gaa gaa ttt aag aaa ttg gtg cag 486
76 Pro Asn Thr Asn Leu Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln
77 135 140 145
79 cac aag gga ctc tcg gag gag gac att ttc atg ccc ctg cag acg gga 534
80 His Lys Gly Leu Ser Glu Glu Asp Ile Phe Met Pro Leu Gln Thr Gly
81 150 155 160
83 agc tgc gtt ctc gaa cac taggcagccc ccgggtctgc acctccagag 582
84 Ser Cys Val Leu Glu His
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87 cccaccctac caccagacac agagcccgga ccacctggac ctaccctcca gccatgaccc 642
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93 <211> LENGTH: 170
94 <212> TYPE: PRT
95 <213> ORGANISM: Homo sapiens
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101 Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys
102 20 25 30
104 Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys
105 35 40 45
107 Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala
108 50 55 60
110 Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu
111 65 70 75 80
113 Met Arg Lys Thr Glu Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg
114 85 90 95
116 Lys Leu Ile Tyr Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe
117 100 105 110
119 Tyr Cys Lys Asp Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu
120 115 120 125
122 Val Gly Arg Asn Pro Asn Thr Asn Leu Glu Ala Leu Glu Glu Phe Lys
123 130 135 140
125 Lys Leu Val Gln His Lys Gly Leu Ser Glu Glu Asp Ile Phe Met Pro
126 145 150 155 160
128 Leu Gln Thr Gly Ser Cys Val Leu Glu His
129 165 170
132 <210> SEQ ID NO: 3
133 <211> LENGTH: 725

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134 <212> TYPE: DNA
135 <213> ORGANISM: Homo sapiens
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138 <221> NAME/KEY: CDS
139 <222> LOCATION: (43)..(480)
141 <220> FEATURE:
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147                                     1
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150 Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala Leu Ser Phe Thr Leu
151   5                               10                               15                               20
153 gag gag gag gat atc aca ggg acc tgg tac gtg aag gcc atg gtg gtc      150
154 Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys Ala Met Val Val
155                               25                               30                               35
157 gat aag gac ttt ccg gag gac agg agg ccc agg aag gtg tcc cca gtg      198
158 Asp Lys Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys Val Ser Pro Val
159                               40                               45                               50
161 aag gtg aca gcc ctg ggc ggt ggg aac ttg gaa gcc acg ttc acc ttc      246
162 Lys Val Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala Thr Phe Thr Phe
163                               55                               60                               65
165 atg agg gag gat cgg tgc atc cag aag aaa atc ctg atg cgg aag acg      294
166 Met Arg Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu Met Arg Lys Thr
167                               70                               75                               80
169 gag gag cct ggc aaa ttc agc gcc tat ggg ggc agg aag ctc ata tac      342
170 Glu Glu Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg Lys Leu Ile Tyr
171   85                               90                               95                               100
173 ctg cag gag ctg ccc ggg acg gac gac tac gtc ttt tac tgc aaa gac      390
174 Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe Tyr Cys Lys Asp
175                               105                               110                               115
177 cag cgc cgt ggg ggc ctg cgc tac atg gga aag ctt gtg ggg ccg tgc      438
178 Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu Val Gly Pro Cys
179                               120                               125                               130
181 cgc tgt ccc cac gtc ggc tca cct ggc cac ctc acc tgc agg      480
182 Arg Cys Pro His Val Gly Ser Pro Gly His Leu Thr Cys Arg
183                               135                               140                               145
185 taggaatcct aataccaacc tggaggccct ggaagaattt aagaaattgg tgcagcacia 540
187 gggactctcg gaggaggaca ttttcatgcc cctgcagacg ggaagctgcg ttctcgaaca 600
189 ctaggcagcc cccgggtctg cacctccaga gccacccta ccaccagaca cagagcccg 660
191 accacctgga cctaccctcc agccatgacc ctccctgct cccaccacc tgactccaaa 720
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197 <211> LENGTH: 146
198 <212> TYPE: PRT
199 <213> ORGANISM: Homo sapiens
201 <400> SEQUENCE: 4
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203   1               5               10               15
205 Ser Phe Thr Leu Glu Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys
206               20               25               30
208 Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys
209               35               40               45
211 Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala
212               50               55               60
214 Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu
215   65               70               75               80
217 Met Arg Lys Thr Glu Glu Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg
218               85               90               95
220 Lys Leu Ile Tyr Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe :
221               100               105               110
223 Tyr Cys Lys Asp Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu :
224               115               120               125
226 Val Gly Pro Cys Arg Cys Pro His Val Gly Ser Pro Gly His Leu Thr
227   130               135               140
229 Cys Arg
230 145
234 <210> SEQ ID NO: 5
235 <211> LENGTH: 741
236 <212> TYPE: DNA
237 <213> ORGANISM: Homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: CDS
241 <222> LOCATION: (43)..(726)
243 <220> FEATURE:
244 <223> OTHER INFORMATION: cDNA396 (741) /SM4 (hOBPIIa-gamma)
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248                                     Met Lys Thr Leu
249                                     1
251 ttc ctg ggt gtc acg ctc ggc ctg gcc gct gcc ctg tcc ttc acc ctg   102
252 Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Leu Ser Phe Thr Leu
253   5               10               15               20
255 gag gag gag gat atc aca ggg acc tgg tac gtg aag gcc atg gtg gtc   150
256 Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys Ala Met Val Val
257               25               30               35
259 gat aag gac ttt ccg gag gac agg agg ccc agg aag gtg tcc cca gtg   198
260 Asp Lys Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys Val Ser Pro Val
261               40               45               50
263 aag gtg aca gcc ctg ggc ggt ggg aac ttg gaa gcc acg ttc acc ttc   246
264 Lys Val Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala Thr Phe Thr Phe
265               55               60               65
267 atg agg gag gat cgg tgc atc cag aag aaa atc ctg atg cgg aag acg   294
268 Met Arg Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu Met Arg Lys Thr
269               70               75               80
271 gag gag cct ggc aaa ttc agc gcc tat ggg ggc agg aag ctc ata tac   342
272 Glu Glu Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg Lys Leu Ile Tyr

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Input Set : A:\65691270.app

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273 85          90          95          100
275 ctg cag gag ctg ccc ggg acg gac gac tac gtc ttt tac tgc aaa gac 390
276 Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe Tyr Cys Lys Asp
277          105          110          115
279 cag cgc cgt ggg ggc ctg cgc tac atg gga aag ctt gtg gca tct gct 438
280 Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu Val Ala Ser Ala
281          120          125          130
283 ccc tgc agg gcc gtg ccg ctg tcc cca cgt cgg ctc acc tgg cca cct 486
284 Pro Cys Arg Ala Val Pro Leu Ser Pro Arg Arg Leu Thr Trp Pro Pro
285          135          140          145
287 cac ctg cag gta gga atc cta ata cca acc tgg agg ccc tgg aag aat 534
288 His Leu Gln Val Gly Ile Leu Ile Pro Thr Trp Arg Pro Trp Lys Asn
289          150          155          160
291 tta aga aat tgg tgc agc aca agg gac tct cgg agg agg aca ttt tca 582
292 Leu Arg Asn Trp Cys Ser Thr Arg Asp Ser Arg Arg Arg Thr Phe Ser
293 165          170          175          180
295 tgc ccc tgc aga cgg gaa gct gcg ttc tcg aac act agg cag ccc ccg 630
296 Cys Pro Cys Arg Arg Glu Ala Ala Phe Ser Asn Thr Arg Gln Pro Pro
297          185          190          195
299 ggt ctg cac ctc cag agc cca ccc tac cac cag aca cag agc ccg gac 678
300 Gly Leu His Leu Gln Ser Pro Pro Tyr His Gln Thr Gln Ser Pro Asp
301          200          205          210
303 cac ctg gac cta ccc tcc agc cat gac cct tcc ctg ctc cca ccc acc 726
304 His Leu Asp Leu Pro Ser Ser His Asp Pro Ser Leu Leu Pro Pro Thr
305          215          220          225
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310 <210> SEQ ID NO: 6
311 <211> LENGTH: 228
312 <212> TYPE: PRT
313 <213> ORGANISM: Homo sapiens
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319 Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr Val Lys
320 20 25 30
322 Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg Pro Arg Lys
323 35 40 45
325 Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly Asn Leu Glu Ala
326 50 55 60
328 Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile Gln Lys Lys Ile Leu
329 65 70 75 80
331 Met Arg Lys Thr Glu Glu Pro Gly Lys Phe Ser Ala Tyr Gly Gly Arg
332 85 90 95
334 Lys Leu Ile Tyr Leu Gln Glu Leu Pro Gly Thr Asp Asp Tyr Val Phe
335 100 105 110
337 Tyr Cys Lys Asp Gln Arg Arg Gly Gly Leu Arg Tyr Met Gly Lys Leu
338 115 120 125
340 Val Ala Ser Ala Pro Cys Arg Ala Val Pro Leu Ser Pro Arg Arg Leu
341 130 135 140

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RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\65691270.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 8507,10635,10643

VERIFICATION SUMMARY

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TIME: 15:30:17

Input Set : A:\65691270.app

Output Set: N:\CRF4\11062002\J049372.raw

L:919 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:8460
L:955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:10620